

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

(A) NAME: MOGEN International nv
(B) STREET: Einsteinweg 97
(C) CITY: Leiden
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 2333 CB
(G) TELEPHONE: 31-(0)71-5258282
(H) TELEFAX: 31-(0)71-5221471

(A) NAME: Gist-brocades N.V.
(B) STREET: Postbus 1
(C) CITY: Delft
(E) COUNTRY: The Netherlands
(F) POSTAL CODE (ZIP): 2600 MA
(G) TELEPHONE: 31-(0)15-2799111
(H) TELEFAX: 31-(0)15-2793957

(ii) TITLE OF INVENTION: Improved process for the production of
alcoholic beverages using Maltseed

(iii) NUMBER OF SEQUENCES: 8

(iv) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)

(vi) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER: EP 96202195.2
(B) FILING DATE: 05-AUG-1996

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 558 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(ix) FEATURE:

(A) NAME/KEY: CDS

(B) LOCATION: 1..558

(D) OTHER INFORMATION: /product= "mature protein"

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

5	ATG AGC GCG GGA ATC AAC TAC GTC CAG AAC TAC AAT GGC AAC CTC GGC	48
	Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly	
	1 5 10 15	
10	GAC TTT ACT TAC GAC GAG TCA GCG GGA ACT TTC AGC ATG TAT TGG GAG	96
	Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu	
	20 25 30	
15	GAT GGC GTG TCC TCA GAC TTC GTC GTG GGA CTG GGC TGG ACC ACT GGA	144
	Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly	
	35 40 45	
20	TCA TCC AAT GCG ATC ACC TAC AGC GCC GAG TAC TCC GCG TCA GGA TCA	192
	Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser	
	50 55 60	
25	GCC TCC TAT CTG GCC GTG TAC GGA TGG GTG AAC TAC CCG CAG GCC GAG	240
	Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu	
	65 70 75 80	
30	TAC TAC ATC GTG GAG GAT TAC GGA GAT TAC AAC CCA TGC AGC TCA GCG	288
	Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala	
	85 90 95	
35	ACC TCC CTC GGA ACT GTG TAC AGC GAC GGC TCC ACC TAC CAG GTC TGC	336
	Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys	
	100 105 110	
40	ACC GAC ACC CGC ACT AAC GAG CCG TCA ATC ACC GGC ACT TCC ACC TTC	384
	Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe	
	115 120 125	
45	ACC CAG TAC TTC AGC GTG CGC GAG TCC ACT CGC ACC TCA GGA ACC GTG	432
	Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val	
	130 135 140	
50	ACC GTC GCG AAC CAC TTC AAC TTC TGG GCG CAG CAC GGA TTC GGC AAC	480
	Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn	
	145 150 155 160	
55	AGC GAC TTT AAC TAC CAG GTG GTC GCA GTG GAG GCA TGG TCA GGA GCG	528
	Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala	
	165 170 175	
60	GGC TCA GCG TCC GTC ACT ATC AGC TCC TG	558
	Gly Ser Ala Ser Val Thr Ile Ser Ser	
	180 185	

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 185 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

Met Ser Ala Gly Ile Asn Tyr Val Gln Asn Tyr Asn Gly Asn Leu Gly
 1 5 10 15

Asp Phe Thr Tyr Asp Glu Ser Ala Gly Thr Phe Ser Met Tyr Trp Glu
 20 25 30

Asp Gly Val Ser Ser Asp Phe Val Val Gly Leu Gly Trp Thr Thr Gly
 35 40 45

Ser Ser Asn Ala Ile Thr Tyr Ser Ala Glu Tyr Ser Ala Ser Gly Ser
 50 55 60

Ala Ser Tyr Leu Ala Val Tyr Gly Trp Val Asn Tyr Pro Gln Ala Glu
 65 70 75 80

Tyr Tyr Ile Val Glu Asp Tyr Gly Asp Tyr Asn Pro Cys Ser Ser Ala
 85 90 95

Thr Ser Leu Gly Thr Val Tyr Ser Asp Gly Ser Thr Tyr Gln Val Cys
 100 105 110

Thr Asp Thr Arg Thr Asn Glu Pro Ser Ile Thr Gly Thr Ser Thr Phe
 115 120 125

Thr Gln Tyr Phe Ser Val Arg Glu Ser Thr Arg Thr Ser Gly Thr Val
 130 135 140

Thr Val Ala Asn His Phe Asn Phe Trp Ala Gln His Gly Phe Gly Asn
 145 150 155 160

Ser Asp Phe Asn Tyr Gln Val Val Ala Val Glu Ala Trp Ser Gly Ala
 165 170 175

Gly Ser Ala Ser Val Thr Ile Ser Ser
 180 185

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

5 (iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(vi) ORIGINAL SOURCE:

10 (A) ORGANISM: Nicotiana tabacum

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 3:

15 AACTTCCTCA AGAGCTTCCC CTTTATGCC TTCCTTTGTT TTGGCCAATA CTTTGTAGCT 60
GTTACGCATG C 71

(2) INFORMATION FOR SEQ ID NO: 4:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

30 (iii) ANTI-SENSE: YES

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

35 CCATGGCATG CGTAACAGCT ACAAAGTATT GGCCAAAACA AAGGAAGGCA TAAAAGGGGA 60
AGCTCTTGAG GAAGTTCATG 80

(2) INFORMATION FOR SEQ ID NO: 5:

40 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 21 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

45

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

50 (iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 5:

ATGGATGGCA TGCTGTTGTA G 21

(2) INFORMATION FOR SEQ ID NO: 6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 6:

GCACAATTCT CGAGGAGACC G

21

(2) INFORMATION FOR SEQ ID NO: 7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 7:

CCTCTTAAGG ATCCAATGCG G

21

(2) INFORMATION FOR SEQ ID NO: 8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(iii) HYPOTHETICAL: NO

(iii) ANTI-SENSE: NO

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 8:

CTTATCTGAA TTCGGAAGCT C

21